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Cryptococcus gattii Risk for Tourists Visiting Vancouver Island, Canada

To the Editor: An unprecedented outbreak of Cryptococcus gattii genotype amplified fragment length polymorphism (AFLP) 6/VGII Vancouver Island, British Columbia, Canada, is affecting both human and animal hosts with normal immunity (1-3). So far, >100 human cases, including at least 6 fatalities, have been reported by the British Columbia Centre for Disease Control (4), (www.bccdc.org, www.cbc.ca). Vancouver Island is a major tourist destination, with ≈7.5 million visits each year (www.bcstats.gov.bc.ca). We report the first known intercontinental transmission of C. gattii from this outbreak in a tourist from Denmark who visited Vancouver Island. This case indicates a potential risk for tourismrelated acquisition.

A 51-year-old, HIV-negative, apparently immunocompetent man from Denmark, with known psoriatic gout and under treatment with a nonsteroidial antiinflammatory drug, was admitted to a hospital in Herning, Denmark, with chest pain radiating to the left shoulder and arm, lasting for 1 day. Six weeks before his admission, he returned to Denmark from a 3week trip to Canada, during which he visited Victoria and surrounding areas on the eastern coast of Vancouver Island for 7 days. During their stay, the patient and his 3 fellow travelers visited gardens and studied the local natural vegetation.

During his stay in Canada, the patient had no symptoms, and symptoms had not developed in any of his family members as of October 2006. On admission to the hospital, his temperature was 38.2°C, and a chest radiograph showed 3 large nodular infiltrates suspect for malignancy or abscesses. Neither bacterial nor

fungal pathogens could be isolated from sputum by classic and molecular methods. After 4-5 days, his temperature was 40°C, a productive cough with dyspnea was noted, and his condition deteriorated. A chest radiograph showed progression of the infiltrates, and a computed tomography scan of the abdomen and chest showed infiltrates near the pleura, suggesting encapsulated fluid (Figure). An ultrasound-guided lung biopsy was performed, and mucoid material was aspirated. Microscopy and a culture from the aspirate showed a cryptococcal isolate. This isolate was further identified by internal transcribed spacer and D1/D2 sequencing, as well as amplified fragment-length polymorphism analysis (2). In addition, detailed genotyping was performed by using sequences of 7 genes (IGS, CAP10, GPD1, LAC1, MPD1, PLB1, and TEF1; GenBank accession nos. DQ861593-DQ861599) (5).

Extensive molecular research showed that this isolate belonged to the highly virulent AFLP genotype 6A (VGIIa) of *Cryptococcus gattii*, which is the major genotype involved in the Vancouver Island *C. gattii* outbreak (1–4). All 7 sequenced genes had a complete match with the sequence types specific for isolates involved in the Vancouver Island outbreak (5). Thus, we conclude that the pathogen was acquired during the patient's visit

to Vancouver Island and imported to Denmark. The presence of 3 cryptococcal masses of more or less equal size suggests that the patient was exposed to a high concentration of infectious cells of C. gattii. The observed incubation time of 6 weeks is shorter than that was previously reported for infections related to the Vancouver Island outbreak (2–11 mo) (4). These observations, in combination with the absence of any known predisposing factor in this patient, such as smoking or treatment with corticosteroids, suggest that this specific AFLP6 genotype of C. gattii is highly virulent (4,5).

This case suggests a potential risk of tourists acquiring cryptococcosis while visiting Vancouver Island. Therefore, we recommend tourists and medical staff of healthcare centers worldwide be alert for symptoms of cryptococcosis after travel to Vancouver Island.

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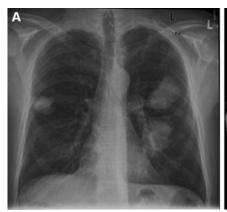




Figure. A) Chest radiograph and B) computed tomographic scan of the patient showing 3 nodular *Cryptococcus gattii* infiltrates near pleura.

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Clostridium difficile in Discharged Inpatients, Germany

To the Editor: Using discharge diagnoses from US hospitals in 2000–2003, McDonald et al. recently documented a dramatic increase in the rate of *Clostridium difficile*—associated disease (CDAD) (1). During the same period, a new strain of *C. difficile* was identified; this strain appears more virulent, at least in part because it produces higher levels of toxin (2).

To our knowledge, this strain has not been identified in Germany. However, to address this emerging threat, we conducted a similar analy-